CRF Errors Corrected by the STIC Systems Branch

Serial Number: 08/162,407

CRF Processing Date: 12/23/93
Edited by: _____
Verified by: _____ (STIC staff)

☐ Changed a file from non-ASCII to ASCII

☑ Changed the margins in cases where the sequence text was "wrapped" down to the next line

☐ Edited a format error in the Current Application Data section, specifically:
_____

ENTERED

☐ Edited the Current Application Data section with the actual current number. The number inputted by the applicant was ☐ the prior application data; or ☐ other _____.

☐ Added the mandatory heading and subheadings for "Current Application Data".

☐ Edited the "Number of Sequences" field. The applicant spelled out a number instead of using an integer.

☐ Changed the spelling of a mandatory field (the headings or subheadings), specifically:
_____

☐ Inserted a space between the last nucleic designator and the nucleic number for sequences:
_____

☐ Deleted page numbers in the text of the sequence listing, which is considered invalid text.

☐ Corrected the SEQ ID NO when obviously incorrect. The sequence numbers that were edited were:
_____

☐ Inserted a nucleic number at the end of a nucleic line. SEQ ID NO's edited:
_____

☐ Corrected subheading placement. All responses must be on the same line as each subheading. If the applicant placed a response below the subheading, this was moved to its appropriate place.

☐ Inserted colons after headings/subheadings. Headings edited included:
_____

☐ Deleted extra, invalid, headings used by an applicant, specifically:
_____

☐ Deleted non-ASCII "garbage" at the end of files, and other invalid text, such as a secretary's initials.

☐ Inserted mandatory headings, specifically: _____

☐ Corrected an obvious error in the response, specifically:
_____

☐ Edited identifiers where upper case is used but lower case is required, or vice versa.

☐ Corrected an error in the Number of Sequences field, specifically:
_____

☐ A "Hard Page Break" code was inserted by the applicant. All occurrences had to be deleted.

☐ Other:
_____
_____

*Examiner: **The above corrections must be communicated to the applicant in the first Office Action. DO NOT send a copy of this form.**   8/01/93

PAGE: 1

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/162,407*

DATE: 12/23/93
TIME: 15:10:15

INPUT SET: S1194.raw

CL

wrapped text

```
 1                               SEQUENCE LISTING
 2
 3   (1)      General Information:
 4            (i) APPLICANT: Lyman, Stewart D.
 5                           Beckmann, M. Patricia
 6
 7            (ii) TITLE OF INVENTION: Ligands for flt3/flk-2 Receptors
 8
 9            (iii) NUMBER OF SEQUENCES: 8
10
11            (iv) CORRESPONDENCE ADDRESS:
12                 (A) ADDRESSEE: Stephen L. Malaska, Immunex Corporation
13                 (B) STREET: 51 University Street
14                 (C) CITY: Seattle
15                 (D) STATE: Washington
16                 (E) COUNTRY: US
17                 (F) ZIP: 98101
18
19            (v) COMPUTER READABLE FORM:
20                 (A) MEDIUM TYPE: Floppy disk
21                 (B) COMPUTER: Apple Macintosh
22                 (C) OPERATING SYSTEM: Macintosh 7.0.1
23                 (D) SOFTWARE: Microsoft Word, Version #5.1
24
25            (vi) CURRENT APPLICATION DATA:
26                 (A) APPLICATION NUMBER: -to be assigned-
27                 (B) FILING DATE:  December 3, 1993
28                 (C) CLASSIFICATION:
29
30            (vii) PRIOR APPLICATION DATA:
31                 (A) APPLICATION NUMBER: 08/111,758
32                 (B) FILING DATE:  August 25, 1993
33                 (C) CLASSIFICATION:
34
35            (vii) PRIOR APPLICATION DATA:
36                 (A) APPLICATION NUMBER: 08/106,463
37                 (B) FILING DATE:  August 12, 1993
38                 (C) CLASSIFICATION:
39
40            (vii) PRIOR APPLICATION DATA:
41                 (A) APPLICATION NUMBER:  08/068,394
42                 (B) FILING DATE:  May 24, 1993
43                 (C) CLASSIFICATION:
44
45            (viii) ATTORNEY/AGENT INFORMATION:
46                 (A) NAME: Malaska, Stephen L.
47                 (B) REGISTRATION NUMBER: 32,655
48                 (C) REFERENCE/DOCKET NUMBER: 2813-C
49
50            (ix) TELECOMMUNICATION INFORMATION:
51                 (A) TELEPHONE: (206) 587-0430
```

--> 26

--> 33

--> 38

--> 43

PAGE: 2

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/162,407*

DATE: 12/23/93
TIME: 15:10:21

INPUT SET: S1194.raw

```
52              (B)  TELEFAX:  (206) 233-0644
53              (C)  TELEX:  756822
54
55      (2)  INFORMATION FOR SEQ ID NO:1:
56
57          (i)  SEQUENCE CHARACTERISTICS:
58              (A)  LENGTH: 879 base pairs
59              (B)  TYPE: nucleic acid
60              (C)  STRANDEDNESS: single
61              (D)  TOPOLOGY: linear
62
63          (ii) MOLECULE TYPE: cDNA to mRNA
64
65         (iii) HYPOTHETICAL: NO
66
67          (iv) ANTI-SENSE: NO
68
69          (ix) FEATURE:
70              (A)  NAME/KEY: misc_feature
71              (B)  LOCATION: 1..25
72
73          (ix) FEATURE:
74              (A)  NAME/KEY: misc_feature
75              (B)  LOCATION: 855..879
76
77          (ix) FEATURE:
78              (A)  NAME/KEY: CDS
79              (B)  LOCATION: 57..752
80
81
82          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
83
84      GTCGACTGGA ACGAGACGAC CTGCTCTGTC ACAGGCATGA GGGGTCCCCG
85      GCAGAG         56
86
87      ATG ACA GTG CTG GCG CCA GCC TGG AGC CCA AAT TCC TCC CTG TTG
88      CTG   104
89      Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
90       1               5                  10                  15
91
92      CTG TTG CTG CTG CTG AGT CCT TGC CTG CGG GGG ACA CCT GAC TGT
93      TAC   152
94      Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
95                      20              25                  30
96      TTC AGC CAC AGT CCC ATC TCC TCC AAC TTC AAA GTG AAG TTT AGA
97      GAG   200
98      Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
99              35              40                  45
100
101     TTG ACT GAC CAC CTG CTT AAA GAT TAC CCA GTC ACT GTG GCC GTC
102     AAT   248
```

PAGE: 3

RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/162,407*

DATE: 12/23/93
TIME: 15:10:26

INPUT SET: S1194.raw

```
         103   Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
         104        50                55                60
         105
         106   CTT CAG GAC GAG AAG CAC TGC AAG GCC TTG TGG AGC CTC TTC CTA
   -->   107   GCC    296
         108   Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
         109   65                70                75                80
         110
         111   CAG CGC TGG ATA GAG CAA CTG AAG ACT GTG GCA GGG TCT AAG
   -->   112   ATG CAA    344
         113   Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
         114                  85                90                95
         115
         116   ACG CTT CTG GAG GAC GTC AAC ACC GAG ATA CAT TTT GTC ACC TCA
   -->   117   TGT    392
         118   Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
         119                  100               105               110
         120
         121   ACC TTC CAG CCC CTA CCA GAA TGT CTG CGA TTC GTC CAG ACC AAC
   -->   122   ATC    440
         123   Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
         124              115               120               125
         125
         126   TCC CAC CTC CTG AAG GAC ACC TGC ACA CAG CTG CTT GCT CTG AAG
   -->   127   CCC    488
         128   Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
         129        130               135               140
         130
         131   TGT ATC GGG AAG GCC TGC CAG AAT TTC TCT CGG TGC CTG GAG GTG
   -->   132   CAG    536
         133   Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
         134   145               150               155               160
         135
         136   TGC CAG CCG GAC TCC TCC ACC CTG CTG CCC CCA AGG AGT CCC ATA
   -->   137   GCC    584
         138   Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
         139              165               170               175
         140
         141   CTA GAA GCC ACG GAG CTC CCA GAG CCT CGG CCC AGG CAG CTG TTG
   -->   142   CTC    632
         143   Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
         144                  180               185               190
         145
         146   CTG CTG CTG CTG CTG CCT CTC ACA CTG GTG CTG CTG GCA GCC GCC TGG
         147   680
         148   Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
         149              195               200               205
         150
         151   GGC CTT CGC TGG CAA AGG GCA AGA AGG AGG GGG GAG CTC CAC CCT
   -->   152   GGG    728
         153   Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
```

```
154        210                  215                  220
155
156     GTG CCC CTC CCC TCC CAT CCC TAGGATTCGA GCCTTGTGCA
-->  157     TCGTTGACTC        779
158     Val Pro Leu Pro Ser His Pro
159     225                  230
160
161     AGCCAGGGTC TTATCTCGGT TACACCTGTA ATCTCAGCCC TTGGGAGCCC
-->  162     AGAGCAGGAT 839
163
164     TGCTGAATGG TCTGGAGCAG GTCGTCTCGT TCCAGTCGAC
165     879
166
167     (2) INFORMATION FOR SEQ ID NO:2:
168
169            (i) SEQUENCE CHARACTERISTICS:
170                  (A) LENGTH: 231 amino acids
171                  (B) TYPE: amino acid
172                  (D) TOPOLOGY: linear
173
174            (ii) MOLECULE TYPE: protein
175
176
177            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
178
179     Met Thr Val Leu Ala Pro Ala Trp Ser Pro Asn Ser Ser Leu Leu Leu
180      1               5                  10                  15
181
182     Leu Leu Leu Leu Leu Ser Pro Cys Leu Arg Gly Thr Pro Asp Cys Tyr
183              20                  25                  30
184
185     Phe Ser His Ser Pro Ile Ser Ser Asn Phe Lys Val Lys Phe Arg Glu
186          35                  40                  45
187
188     Leu Thr Asp His Leu Leu Lys Asp Tyr Pro Val Thr Val Ala Val Asn
189      50                  55                  60
190
191     Leu Gln Asp Glu Lys His Cys Lys Ala Leu Trp Ser Leu Phe Leu Ala
192     65                  70                  75                  80
193
194     Gln Arg Trp Ile Glu Gln Leu Lys Thr Val Ala Gly Ser Lys Met Gln
195             .      85                  90                  95
196
197     Thr Leu Leu Glu Asp Val Asn Thr Glu Ile His Phe Val Thr Ser Cys
198              100                 105                 110
199
200     Thr Phe Gln Pro Leu Pro Glu Cys Leu Arg Phe Val Gln Thr Asn Ile
201              115                 120                 125
202
203     Ser His Leu Leu Lys Asp Thr Cys Thr Gln Leu Leu Ala Leu Lys Pro
204              130                 135                 140
```

```
205
206   Cys Ile Gly Lys Ala Cys Gln Asn Phe Ser Arg Cys Leu Glu Val Gln
207   145               150               155                   160
208
209   Cys Gln Pro Asp Ser Ser Thr Leu Leu Pro Pro Arg Ser Pro Ile Ala
210                   165               170                   175
211
212   Leu Glu Ala Thr Glu Leu Pro Glu Pro Arg Pro Arg Gln Leu Leu Leu
213               180               185                   190
214
215   Leu Leu Leu Leu Leu Pro Leu Thr Leu Val Leu Leu Ala Ala Ala Trp
216           195               200                   205
217
218   Gly Leu Arg Trp Gln Arg Ala Arg Arg Arg Gly Glu Leu His Pro Gly
219       210               215                   220
220
221   Val Pro Leu Pro Ser His Pro
222   225                   230
223
224          (2) INFORMATION FOR SEQ ID NO:3:
225
226          (i) SEQUENCE CHARACTERISTICS:
227              (A) LENGTH: 24 base pairs
228              (B) TYPE: nucleic acid
229              (C) STRANDEDNESS: single
230              (D) TOPOLOGY: linear
231
232      (iii) HYPOTHETICAL: NO
233
234      (iv) ANTI-SENSE: NO
235
236      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:
237
238   TCGACTGGAA CGAGACGACC TGCT                                    24
239
240
241   (2) INFORMATION FOR SEQ ID NO:4:
242
243          (i) SEQUENCE CHARACTERISTICS:
244              (A) LENGTH: 20 base pairs
245              (B) TYPE: nucleic acid
246              (C) STRANDEDNESS: single
247              (D) TOPOLOGY: linear
248
249      (iii) HYPOTHETICAL: NO
250
251      (iv) ANTI-SENSE: NO
252
253      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:
254
255   AGCAGGTCGT CTCGTTCCAG                                         20
```

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RAW SEQUENCE LISTING
PATENT APPLICATION *US/08/162,407*

DATE: 12/23/93
TIME: 15:10:43

INPUT SET: S1194.raw

```
256
257    (2) INFORMATION FOR SEQ ID NO:5:
258
259        (i) SEQUENCE CHARACTERISTICS:
-->  260            (A) LENGTH: 988 base pairs
261                (B) TYPE: nucleic acid
262                (C) STRANDEDNESS: single
263                (D) TOPOLOGY: linear
264
265        (ii) MOLECULE TYPE: cDNA to mRNA
266
267       (iii) HYPOTHETICAL: NO
268
269        (iv) ANTI-SENSE: NO
270
271        (ix) FEATURE:
272                (A) NAME/KEY: CDS
273                (B) LOCATION: 30..734
274
275        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:
276
277    CGGCCGGAAT TCCGGGGCCC CCGGCCGAA ATG ACA GTG CTG GCG CCA
-->  278    GCC TGG    53
279                                  Met Thr Val Leu Ala Pro Ala Trp
280                                   1               5
281
282    AGC CCA ACA ACC TAT CTC CTC CTG CTG CTG CTG CTG AGC TCG GGA
-->  283    CTC    101
284    Ser Pro Thr Thr Tyr Leu Leu Leu Leu Leu Leu Leu Ser Ser Gly Leu
285        10              15                  20
286
287    AGT GGG ACC CAG GAC TGC TCC TTC CAA CAC AGC CCC ATC TCC TCC
-->  288    GAC    149
289    Ser Gly Thr Gln Asp Cys Ser Phe Gln His Ser Pro Ile Ser Ser Asp
290     25              30                  35                  40
291
292    TTC GCT GTC AAA ATC CGT GAG CTG TCT GAC TAC CTG CTT CAA GAT
-->  293    TAC    197
294    Phe Ala Val Lys Ile Arg Glu Leu Ser Asp Tyr Leu Leu Gln Asp Tyr
295                45                  50                  55
296
297    CCA GTC ACC GTG GCC TCC AAC CTG CAG GAC GAG GAG CTC TGC GGG
-->  298    GGC    245
299    Pro Val Thr Val Ala Ser Asn Leu Gln Asp Glu Glu Leu Cys Gly Gly
300                60                  65                  70
301
302    CTC TGG CGG CTG GTC CTG GCA CAG CGC TGG ATG GAG CGG CTC AAG
-->  303    ACT    293
304    Leu Trp Arg Leu Val Leu Ala Gln Arg Trp Met Glu Arg Leu Lys Thr
305                75                  80                  85
.306
```

INPUT SET: S1194.raw

```
      307   GTC GCT GGG TCC AAG ATG CAA GGC TTG CTG GAG CGC GTG AAC ACG
-->   308   GAG   341
      309   Val Ala Gly Ser Lys Met Gln Gly Leu Leu Glu Arg Val Asn Thr Glu
      310         90              95              100
      311
      312   ATA CAC TTT GTC ACC AAA TGT GCC TTT CAG CCC CCC CCC AGC TGT
-->   313   CTT   389
      314   Ile His Phe Val Thr Lys Cys Ala Phe Gln Pro Pro Pro Ser Cys Leu
      315   105             110         115             120
      316
      317   CGC TTC GTC CAG ACC AAC ATC TCC CGC CTC CTG CAG GAG ACC TCC
-->   318   GAG   437
      319   Arg Phe Val Gln Thr Asn Ile Ser Arg Leu Leu Gln Glu Thr Ser Glu
      320             125         130             135
      321
      322   CAG CTG GTG GCG CTG AAG CCC TGG ATC ACT CGC CAG AAC TTC TCC
-->   323   CGG   485
      324   Gln Leu Val Ala Leu Lys Pro Trp Ile Thr Arg Gln Asn Phe Ser Arg
      325             140             145             150
      326
      327   TGC CTG GAG CTG CAG TGT CAG CCC GAC TCC TCA ACC CTG CCA CCC
-->   328   CCA   533
      329   Cys Leu Glu Leu Gln Cys Gln Pro Asp Ser Ser Thr Leu Pro Pro Pro
      330         155             160             165
      331
      332   TGG AGT CCC CGG CCC CTG GAG GCC ACA GCC CCG ACA GCC CCG CAG
-->   333   CCC   581
      334   Trp Ser Pro Arg Pro Leu Glu Ala Thr Ala Pro Thr Ala Pro Gln Pro
      335         170             175             180
      336
      337   CCT CTG CTC CTC CTA CTG CTG CTG CCC GTG GGC CTC CTG CTG CTG GCC
      338   629
      339   Pro Leu Leu Leu Leu Leu Leu Leu Pro Val Gly Leu Leu Leu Leu Ala
      340   185             190             195             200
      341
      342   GCT GCC TGG TGC CTG CAC TGG CAG AGG ACG CGG CGG AGG ACA CCC
-->   343   CGC   677
      344   Ala Ala Trp Cys Leu His Trp Gln Arg Thr Arg Arg Arg Thr Pro Arg
      345             205             210             215
      346
      347   CCT GGG GAG CAG GTG CCC CCC GTC CCC AGT CCC CAG GAC CTG CTG
-->   348   CTT   725
      349   Pro Gly Glu Gln Val Pro Pro Val Pro Ser Pro Gln Asp Leu Leu Leu
      350             220             225             230
      351
      352   GTG GAG CAC TGACCTGGCC AAGGCCTCAT CCTGCGGAGC CTTAAACAAC
      353   774
      354   Val Glu His
      355             235
      356
      357   GCAGTGAGAC AGACATCTAT CATCCCATTT TACAGGGGAG
```

INPUT SET: S1194.raw

--> **358   GATACTGAGG CACACAGAGG 834**

359

360   GGAGTCACCA GCCAGAGGAT GTATAGCCTG GACACAGAGG

--> **361   AAGTTGGCTA GAGGCCGGTC 894**

362

363   CCTTCCTTGG GCCCCTCTCA TTCCCTCCCC AGAATGGAGG CAACGCCAGA

--> **364   ATCCAGCACC 954**

365

366   GGCCCCATTT ACCCAACTCT GAACAAAGCC CCCG   988

367

368   (2) INFORMATION FOR SEQ ID NO:6:

369

370   (i) SEQUENCE CHARACTERISTICS:

371   (A) LENGTH: 235 amino acids

372   (B) TYPE: amino acid

373   (D) TOPOLOGY: linear

374

375   (ii) MOLECULE TYPE: protein

376

377   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

378

379   Met Thr Val Leu Ala Pro Ala Trp Ser Pro Thr Thr Tyr Leu Leu Leu

380   1   5   10   15

381

382   Leu Leu Leu Leu Ser Ser Gly Leu Ser Gly Thr Gln Asp Cys Ser Phe

383   20   25   30

384

385   Gln His Ser Pro Ile Ser Ser Asp Phe Ala Val Lys Ile Arg Glu Leu

386   35   40   45

387

388   Ser Asp Tyr Leu Leu Gln Asp Tyr Pro Val Thr Val Ala Ser Asn Leu

389   50   55   60

390

391   Gln Asp Glu Glu Leu Cys Gly Gly Leu Trp Arg Leu Val Leu Ala Gln

392   65   70   75   80

393

394   Arg Trp Met Glu Arg Leu Lys Thr Val Ala Gly Ser Lys Met Gln Gly

395   85   90   95

396

397   Leu Leu Glu Arg Val Asn Thr Glu Ile His Phe Val Thr Lys Cys Ala

398   100   105   110

399

400   Phe Gln Pro Pro Pro Ser Cys Leu Arg Phe Val Gln Thr Asn Ile Ser

401   115   120   125

402

403   Arg Leu Leu Gln Glu Thr Ser Glu Gln Leu Val Ala Leu Lys Pro Trp

404   130   135   140

405

406   Ile Thr Arg Gln Asn Phe Ser Arg Cys Leu Glu Leu Gln Cys Gln Pro

407   145   150   155   160

408

```
409   Asp Ser Ser Thr Leu Pro Pro Pro Trp Ser Pro Arg Pro Leu Glu Ala
410               165             170             175
411
412   Thr Ala Pro Thr Ala Pro Gln Pro Pro Leu Leu Leu Leu Leu Leu Leu
413               180             185                 190
414
415   Pro Val Gly Leu Leu Leu Leu Ala Ala Ala Trp Cys Leu His Trp Gln
416           195                 200                 205
417
418   Arg Thr Arg Arg Arg Thr Pro Arg Pro Gly Glu Gln Val Pro Pro Val
419       210                 215                 220
420
421   Pro Ser Pro Gln Asp Leu Leu Leu Val Glu His
422   225             230                 235
423
424   (2) INFORMATION FOR SEQ ID NO:7:
425
426       (i) SEQUENCE CHARACTERISTICS:
427           (A) LENGTH: 71 base pairs
428           (B) TYPE: nucleic acid
429           (C) STRANDEDNESS: single
430           (D) TOPOLOGY: linear
431
432     (ii) MOLECULE TYPE: cDNA to mRNA
433
434    (iii) HYPOTHETICAL: NO
435
436     (iv) ANTI-SENSE: NO
437
438
439
440
441     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:
442
443   AATTGGTACC TTTGGATAAA AGAGACTACA AGGACGACGA
444   TGACAAGACA CCTGACTGTT   60
445
446   ACTTCAGCCA C                                               71
447
448   (2) INFORMATION FOR SEQ ID NO:8:
449
450       (i) SEQUENCE CHARACTERISTICS:
451           (A) LENGTH: 37 base pairs
452           (B) TYPE: nucleic acid
453           (C) STRANDEDNESS: single
454           (D) TOPOLOGY: linear
455
456     (ii) MOLECULE TYPE: cDNA to mRNA
457
458    (iii) HYPOTHETICAL: NO
459
```

```
460        (iv) ANTI-SENSE: NO
461
462
463
464
465        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:
466
467   ATATGGATCC CTACTGCCTG GGCCGAGGCT CTGGGAG
468   37
469
470
471
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION *US/08/162,407*

INPUT SET: S1194.raw

Line	Error	Original Text
26	Wrong application Serial Number	(A) APPLICATION NUMBER: -to be assigned-
33	Unknown or Misplaced Identifier	(C) CLASSIFICATION:
38	Unknown or Misplaced Identifier	(C) CLASSIFICATION:
43	Unknown or Misplaced Identifier	(C) CLASSIFICATION:
58	Entered (879) and Calc. Seq. Length (68) differ	(A) LENGTH: 879 base pairs
85	# of Sequences for line conflicts w/ running total	GCAGAG 56
88	# of Sequences for line conflicts w/ running total	CTG 104
93	# of Sequences for line conflicts w/ running total	TAC 152
97	# of Sequences for line conflicts w/ running total	GAG 200
102	# of Sequences for line conflicts w/ running total	AAT 248
107	# of Sequences for line conflicts w/ running total	GCC 296
112	# of Sequences for line conflicts w/ running total	ATG CAA 344
117	# of Sequences for line conflicts w/ running total	TGT 392
122	# of Sequences for line conflicts w/ running total	ATC 440
127	# of Sequences for line conflicts w/ running total	CCC 488
132	# of Sequences for line conflicts w/ running total	CAG 536
137	# of Sequences for line conflicts w/ running total	GCC 584
142	# of Sequences for line conflicts w/ running total	CTC 632
152	# of Sequences for line conflicts w/ running total	GGG 728
157	# of Sequences for line conflicts w/ running total	TCGTTGACTC 779
162	# of Sequences for line conflicts w/ running total	AGAGCAGGAT 839
260	Entered (988) and Calc. Seq. Length (129) differ	(A) LENGTH: 988 base pairs
278	# of Sequences for line conflicts w/ running total	GCC TGG 53
283	# of Sequences for line conflicts w/ running total	CTC 101
288	# of Sequences for line conflicts w/ running total	GAC 149
293	# of Sequences for line conflicts w/ running total	TAC 197
298	# of Sequences for line conflicts w/ running total	GGC 245
303	# of Sequences for line conflicts w/ running total	ACT 293
308	# of Sequences for line conflicts w/ running total	GAG 341
313	# of Sequences for line conflicts w/ running total	CTT 389
318	# of Sequences for line conflicts w/ running total	GAG 437
323	# of Sequences for line conflicts w/ running total	CGG 485
328	# of Sequences for line conflicts w/ running total	CCA 533
333	# of Sequences for line conflicts w/ running total	CCC 581
343	# of Sequences for line conflicts w/ running total	CGC 677
348	# of Sequences for line conflicts w/ running total	CTT 725
358	# of Sequences for line conflicts w/ running total	GATACTGAGG CACACAGAGG 834
361	# of Sequences for line conflicts w/ running total	AAGTTGGCTA GAGGCCGGTC 894
364	# of Sequences for line conflicts w/ running total	ATCCAGCACC 954
427	Entered (71) and Calc. Seq. Length (31) differ	(A) LENGTH: 71 base pairs
444	# of Sequences for line conflicts w/ running total	TGACAAGACA CCTGACTGTT 60
451	Entered (37) and Calc. Seq. Length (0) differ	(A) LENGTH: 37 base pairs

SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION *US/08/162,407*

INPUT SET: S1194.raw

< < THERE ARE NO ITEMS MISSING > >

SEQUENCE CORRECTION REPORT
PATENT APPLICATION   *US/08/162,407*

INPUT SET: S1194.raw

Line   Original Text   Corrected Text